Please amend the application as follows:

IN THE SPECIFICATION

Please cancel the Sequence Listing submitted with the original application and substitute therefore the Sequence Listing submitted herewith as Exhibit 1.

Please further amend the specification as follows (a "marked up" version of the amendments is attached hereto as Exhibit 2 pursuant to Rule 1.121(b)):

On page 8, replace paragraphs Nos.: [0026]-[0029] with the following:

[0026] Figure 3 shows an alignment of the partial amino acid sequences of CO I from *G. oxydans* DSM 4025 with ones from other organisms. The sequences shown include a peptide sequence obtained from *G. oxydans* DSM 4025 (SEQ ID NO: 11), and an amino acid sequence deduced from the DNA amplified by PCR from *G. oxydans* DSM 4025 (SEQ ID NO: 13), as well as amino acid sequences from *Paracoccus denitrificans* (SEQ ID NO: 19), *Rhodobacter sphaeroides* (SEQ ID NO: 20), and *Bovine* (Mitochondria) (SEQ ID NO: 21).

[0027] Figure 4 shows an alignment of the partial amino acid sequences of CO II from *G. oxydans* DSM 4025 with ones from other organisms. The sequences shown include a peptide sequence obtained from *G. oxydans* DSM 4025 (SEQ ID NO: 14) and an amino acid sequence deduced from the DNA amplified by PCR from *G. oxydans* DSM 4025 (SEQ ID NO: 25), as well as amino acid sequences from *Paracoccus*

denitrificans (SEQ ID NO: 22), *Rhodobacter sphaeroides* (SEQ ID NO: 23), and *Bovine* (Mitochondria) (SEQ ID NO: 24).

[0028] Figure 5 shows an alignment of the partial amino acid sequences of CO III from *G. oxydans* DSM 4025 with those from other organisms. The sequences shown include amino acid sequences deduced from the DNA amplified by PCR from *G. oxydans* DSM 4025 (SEQ ID NOs: 29 and 30), as well as amino acid sequences from *Paracoccus denitrificans* (SEQ ID NO: 26), *Rhodobacter sphaeroides* (SEQ ID NO: 27), and *Bovine* (Mitochondria) (SEQ ID NO: 28).

A2

[0029] Figure 6 shows primers for PCR amplification of the partial CO I, II and III genes of the cytochrome c oxidase complex from *G. oxydans* DSM 4025. The sequences shown include the following: the nucleotide sequence of the CO I (A) primer (SEQ ID NO: 31) and its deduced amino acid sequence (SEQ ID NO: 9); the nucleotide sequence of the CO I (B) primer (SEQ ID NO: 32) and its deduced amino acid sequence (SEQ ID NO: 10); the nucleotide sequence of the CO II (A) primer (SEQ ID NO: 33) and its deduced amino acid sequence (SEQ ID NO: 15); the nucleotide sequence of the CO II (B) primer (SEQ ID NO: 34) and its deduced amino acid sequence (SEQ ID NO: 16); the nucleotide sequence of the CO III (A) primer (SEQ ID NO: 35) and its deduced amino acid sequence (SEQ ID NO: 17); the nucleotide sequence of the CO III (B) primer (SEQ ID NO: 36) and its deduced amino acid sequence (SEQ ID NO: 18).

On page 8, replace paragraph No.: [0031] with the following:

[0031] Figure 8 shows an alignment of the complete amino acid sequence of the CO I subunit from *G. oxydans* DSM 4025 (SEQ ID NO: 2) with those from other organisms. The sequences from other organisms include those from *Bovine* (Mitochondria) (SEQ ID NO: 21), *Paracoccus denitrificans* (SEQ ID NO: 19), and *Rhodobacter sphaeroides* (SEQ ID NO: 20).

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On page 9, replace paragraph No.: [0034] with the following:

[0034] As used herein, the phrase "a biologically and/or taxonomically homogeneous culture of a microorganism having the identifying characteristics of *G. oxydans* DSM 4025" means a microorganism that has at least 12 out of 14 of the following characteristics of *G. oxydans* DSM 4025:

(a) produces 2-KGA from L-sorbose,

(b) oxidizes ethanol to acetic acid,

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(c) oxidizes D-glucose to D-gluconic acid and 2-keto-D-gluconic acid,

(d) exhibits ketogenesis of polyalcohols,

(e) exhibits pellicle and ring growth in mannitol broth (24 hour cultivation) at pH 4 and 5, and pellicle growth in glucose broth at pH 4.5,

(f) does not substantially oxidize glycerol to dihydrooxyacetone,

(g) produces 2-keto-D-glucaric acid from sorbitol and glucaric acid but not from glucose, fructose, gluconic acid, mannitol or 2-keto-D-gluconic acid,

(h) is polymorphic, with no apparent flagella,

(i) produces brown pigment from fructose,

(j) exhibits good growth when co-cultured in the presence of *B. megaterium* or a cell extract thereof,

(k) is streptomycin sensitive,

(l) is rod-shaped with rounded ends,

(m) has an average cell diameter of about 0.3-0.6 micrometers,

(n) has an average cell length of about 1-1.5 micrometers; and

Q4 which microorganism produces 2-KGA from L-sorbose on the level of at least 0.01 g/L of 2-KGA in the culture medium as measured by HPLC. In addition to this, the phrase "a biologically and/or taxonomically homogeneous culture of a microorganism having the identifying characteristics of *G. oxydans* DSM 4025" should be understood to encompass a microorganism comprising a polynucleotide sequence which hybridizes under high stringency conditions to a polynucleotide sequence which encodes a polypeptide selected from the group consisting of SEQ ID NO:2, 4, 6, and 8, as it is obvious for the person skilled in the art that such a microorganism can be identified based on homology of the amino acid sequences.

IN THE CLAIMS

In accordance with amendment practice pursuant to Rule 1.121(c)(1)(i), please enter the "clean" set of "rewritten claims" as set forth below. A "marked up" version of the amended claims is attached hereto as Exhibit 3 pursuant to Rule 1.121(c)(1)(ii).